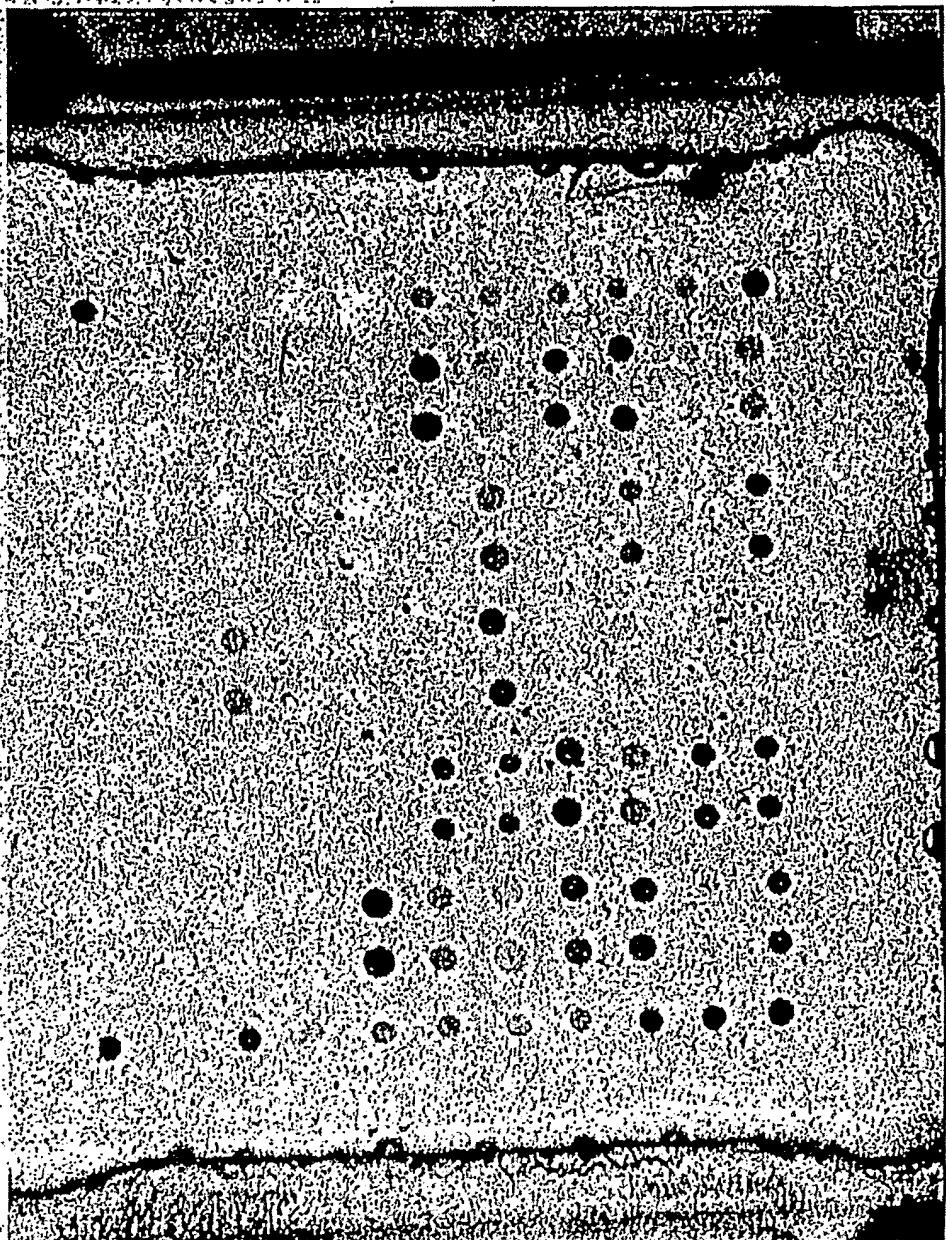


# *P. aeruginosa* AT-Chip

1/30

Fig.1

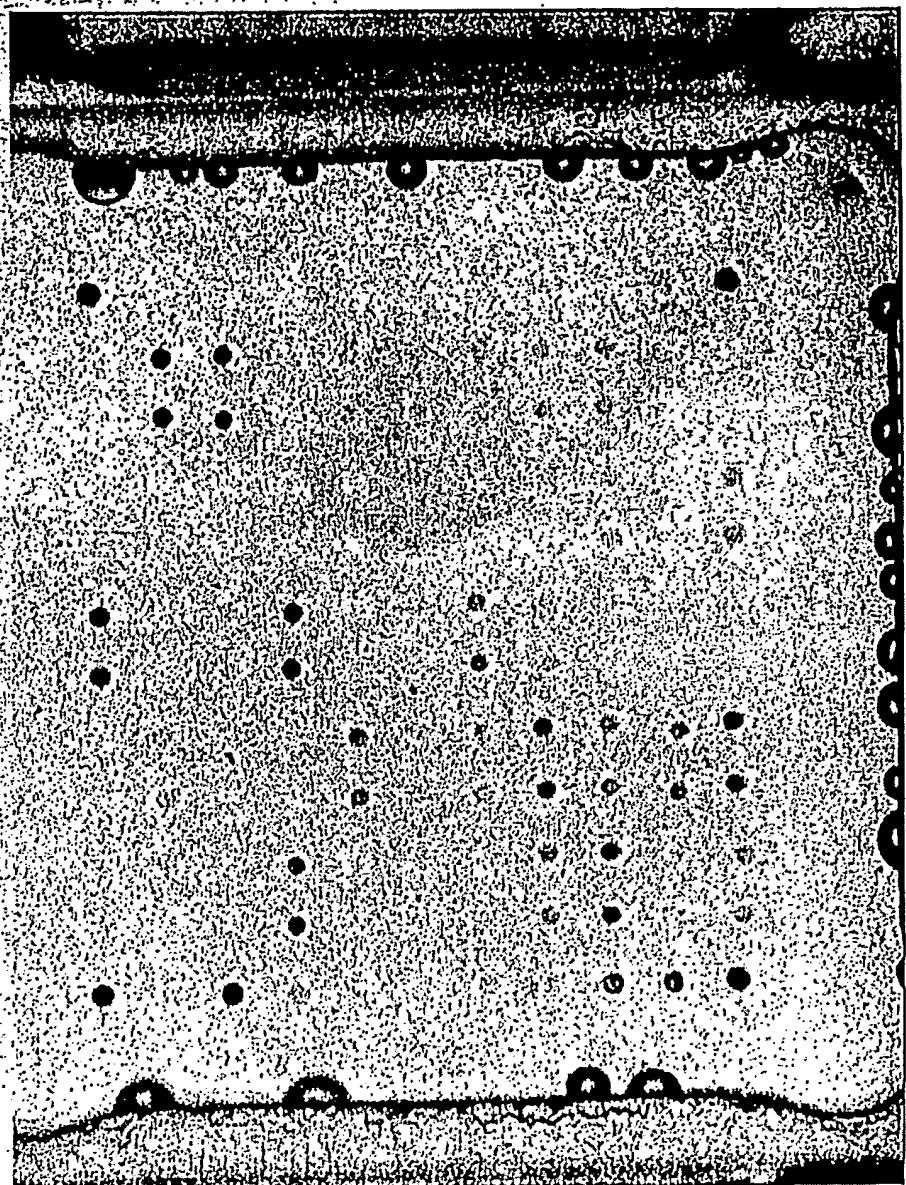


ZW117

*P. aeruginosa* AT-Chip

2/30

Fig.2

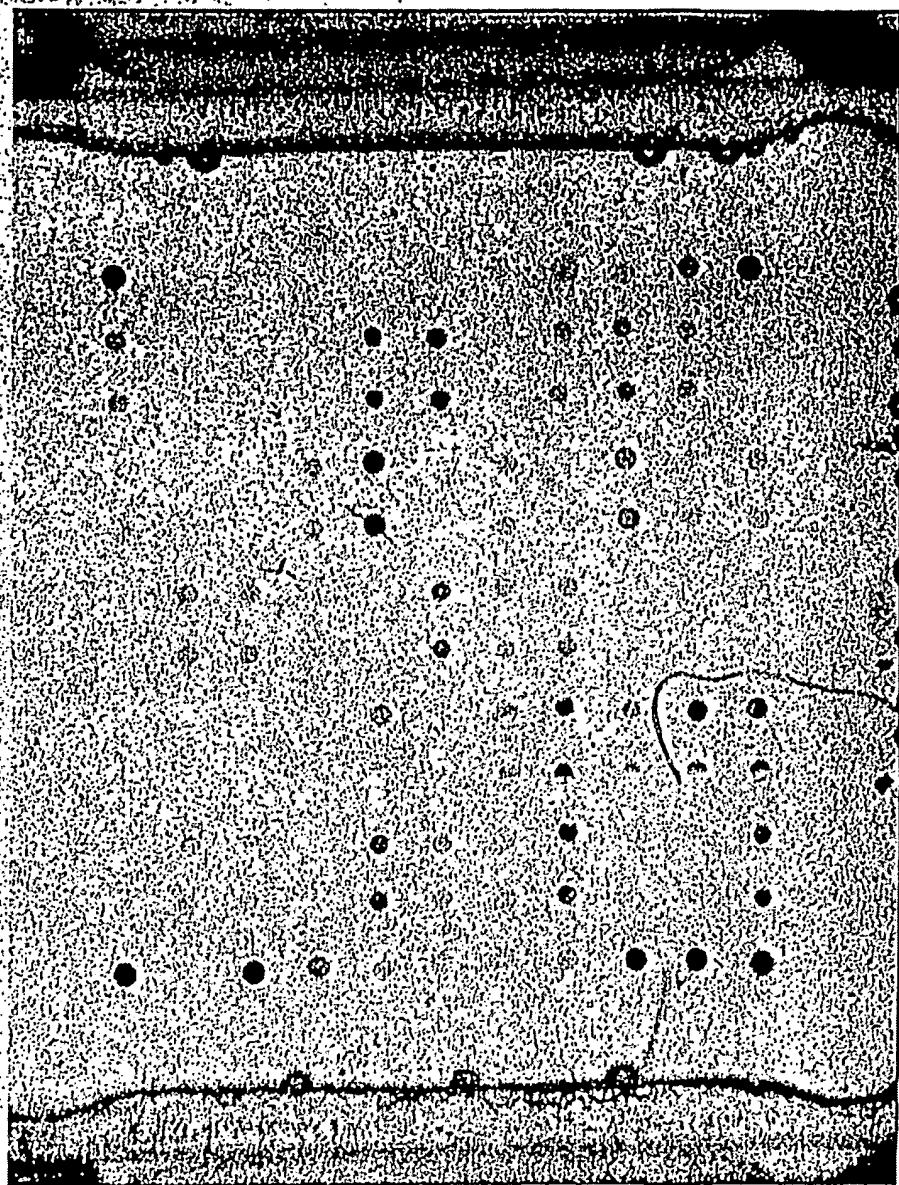


RP17

# *P. aeruginosa* AT-Chip

3/30

Fig.3

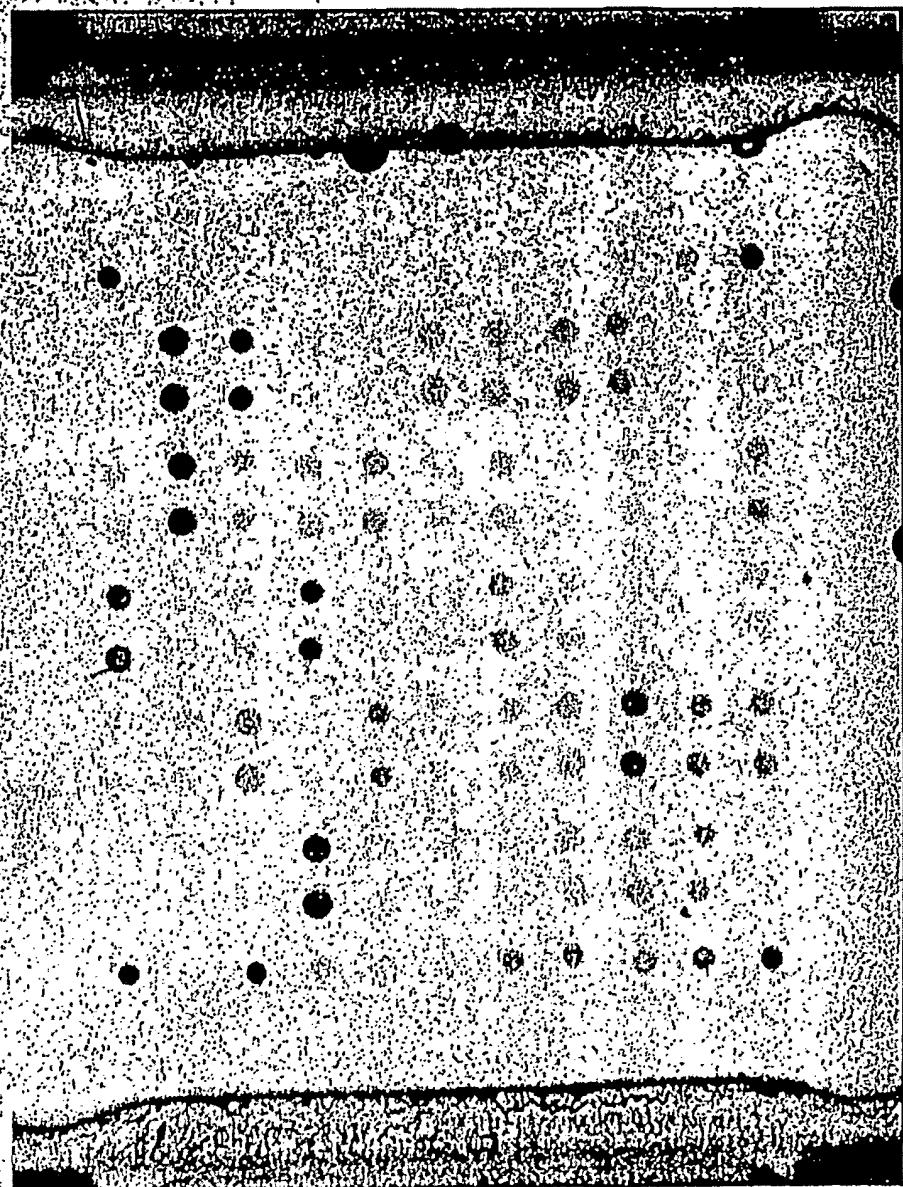


TB

*P. aeruginosa* AT-Chip

4/30

Fig.4

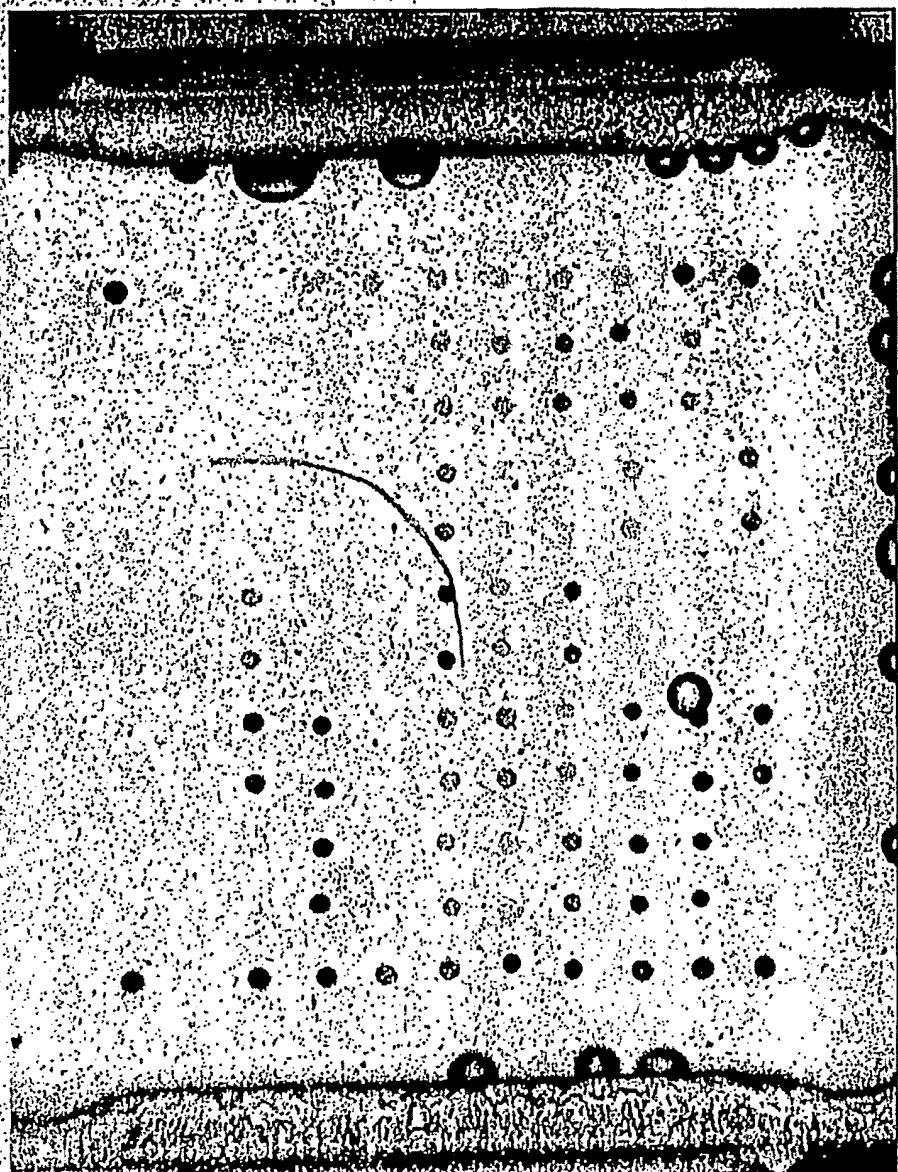


SG17M

# *P. aeruginosa* AT-Chip

5/30

Fig.5

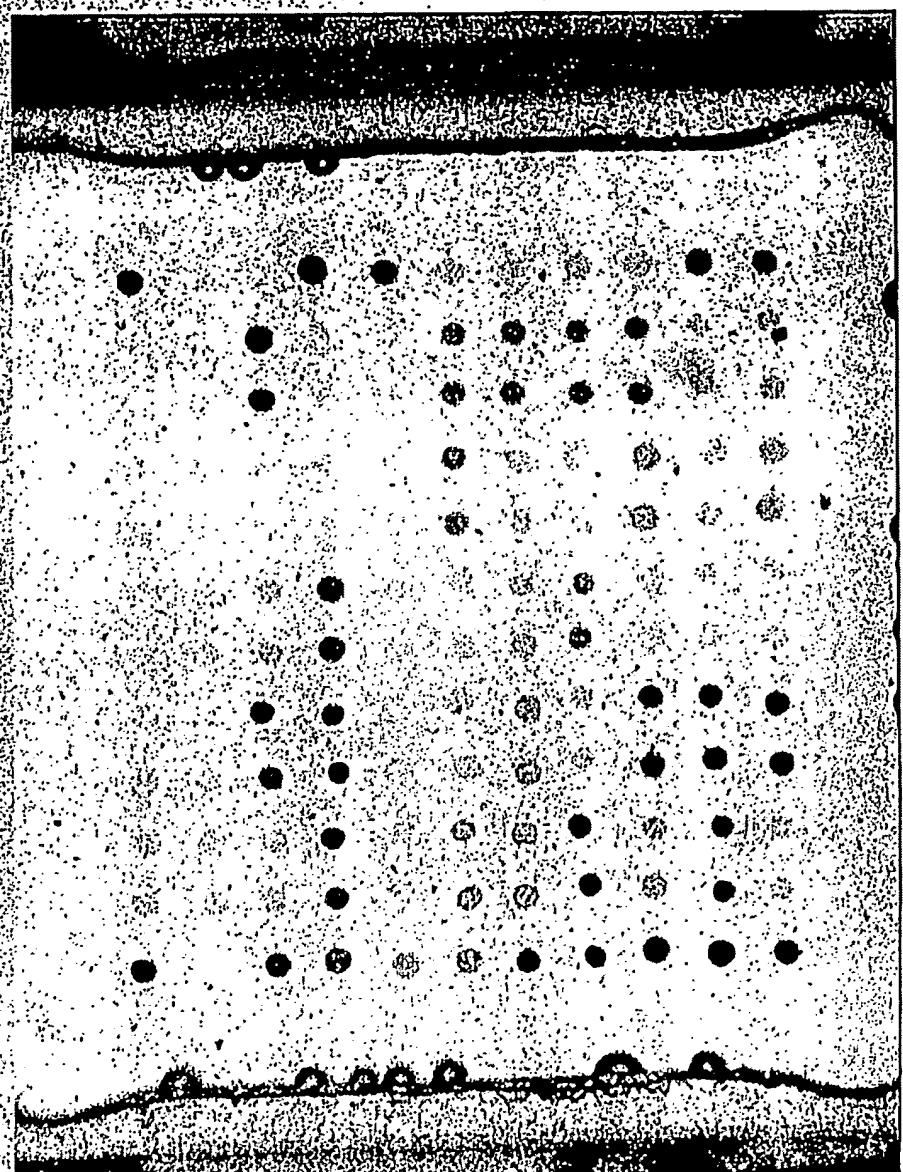


BST85

# *P. aeruginosa* AT-Chip

6/30

Fig.6

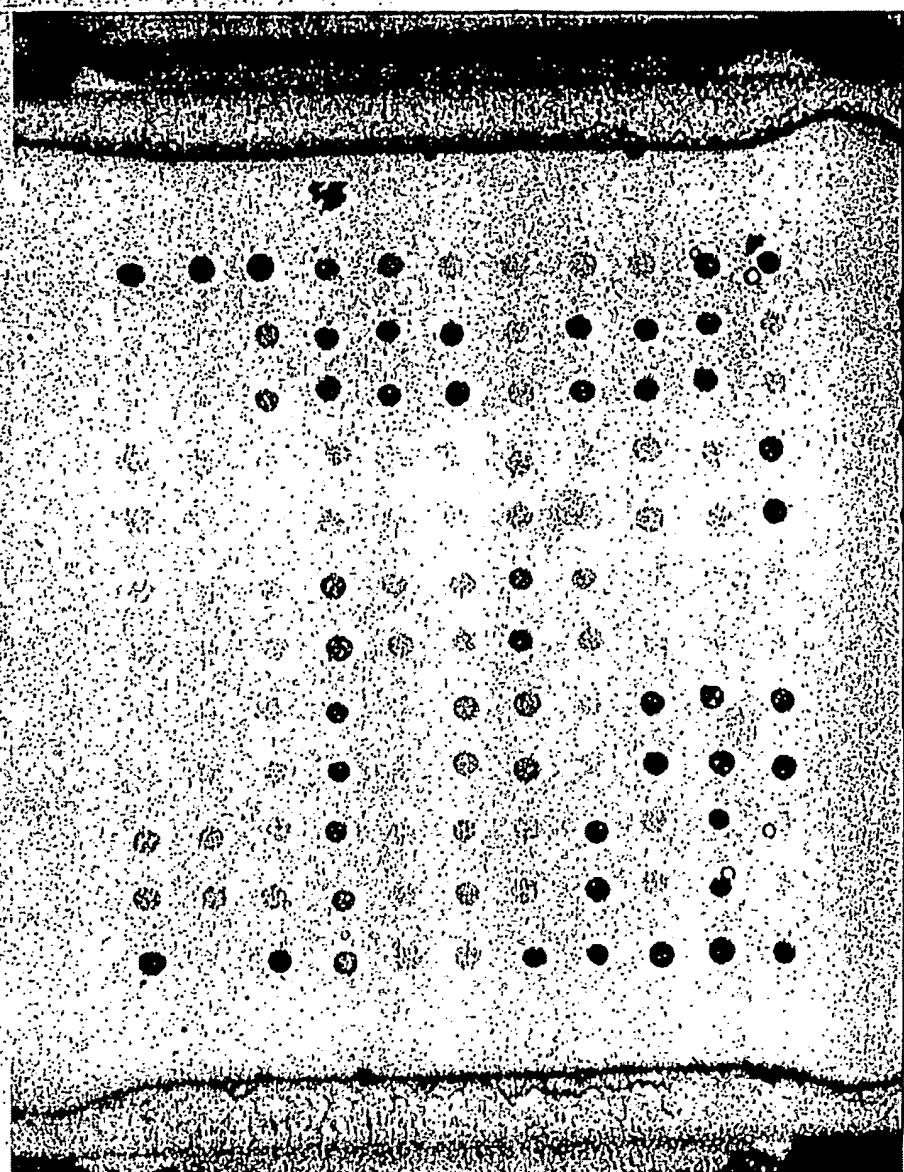


AL 5846

# *P. aeruginosa* AT-Chip

7/30

Fig.7

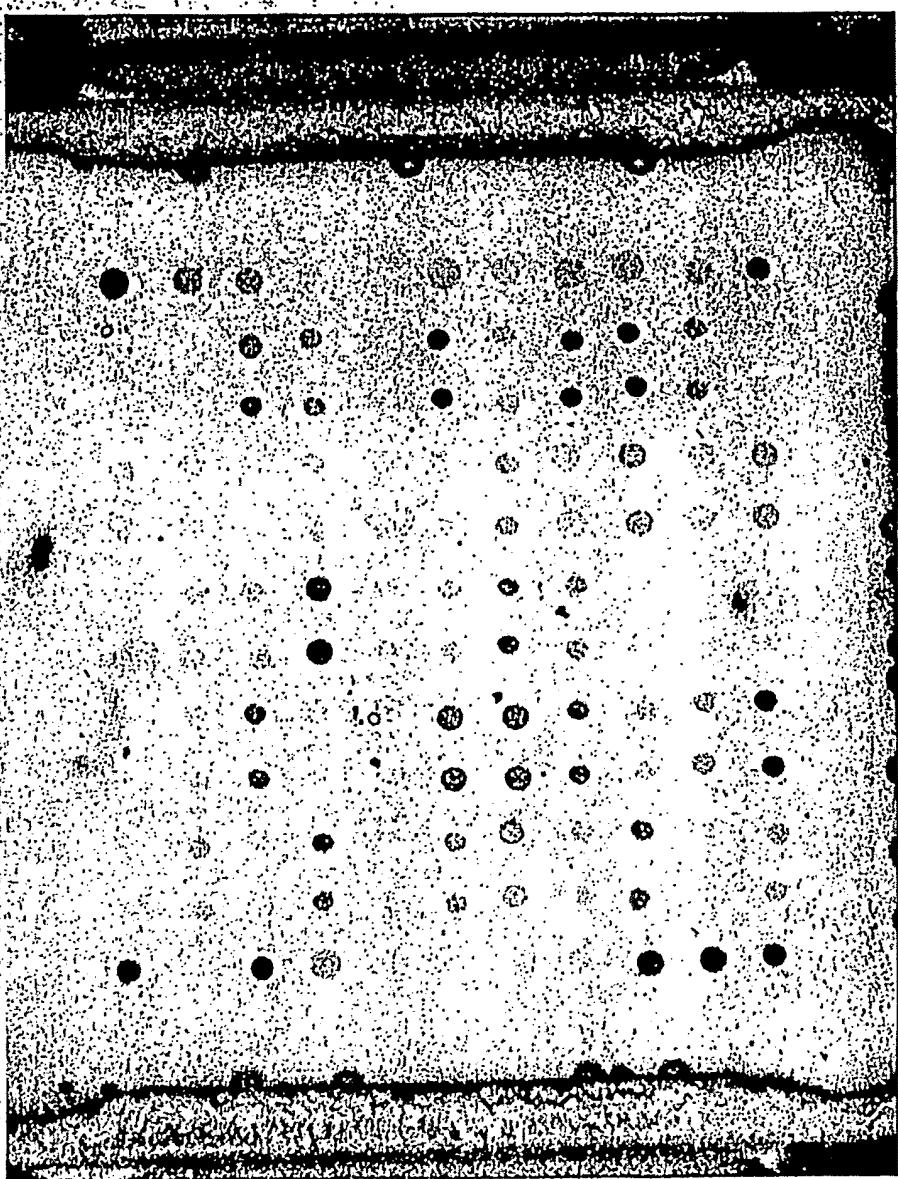


PT12

*P. aeruginosa* AT-Chip

8/30

Fig.8

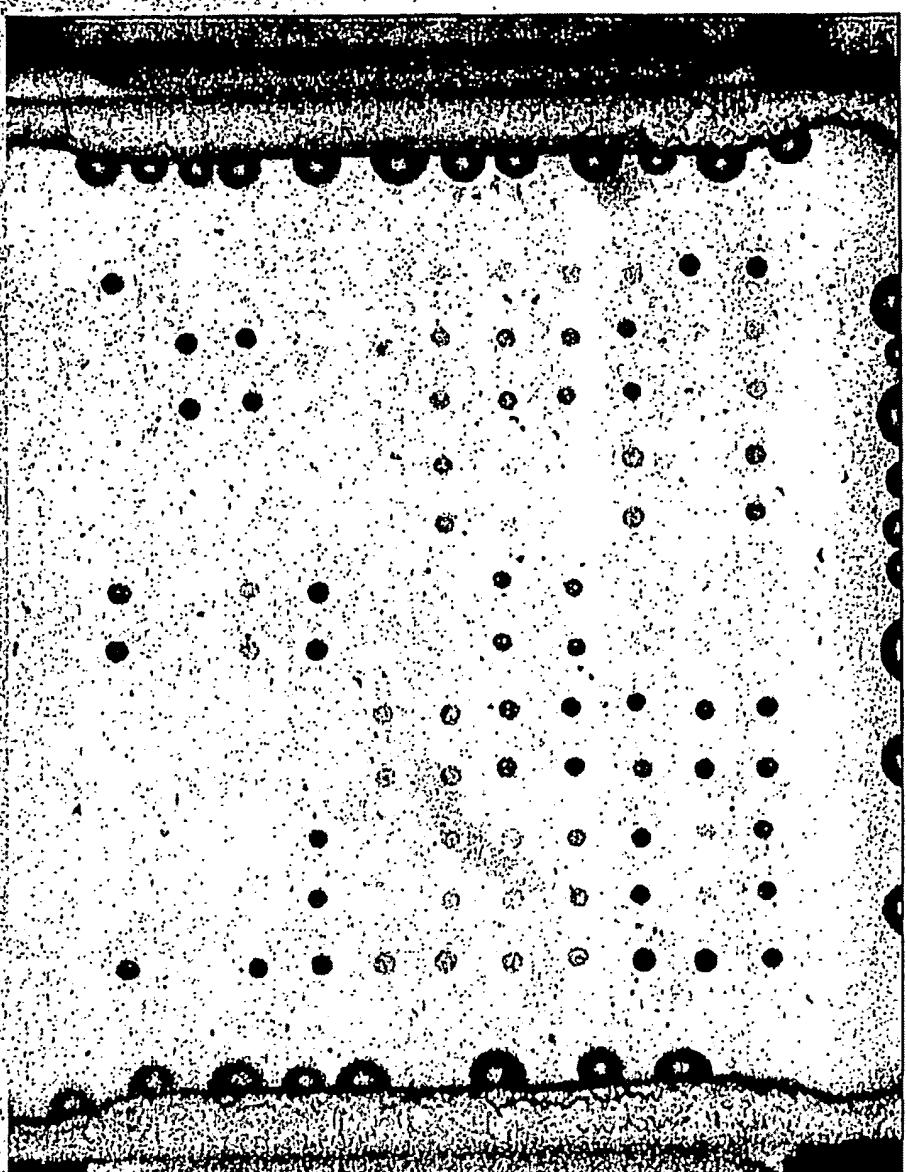


PT20

# *P. aeruginosa* AT-Chip

9/30

Fig.9

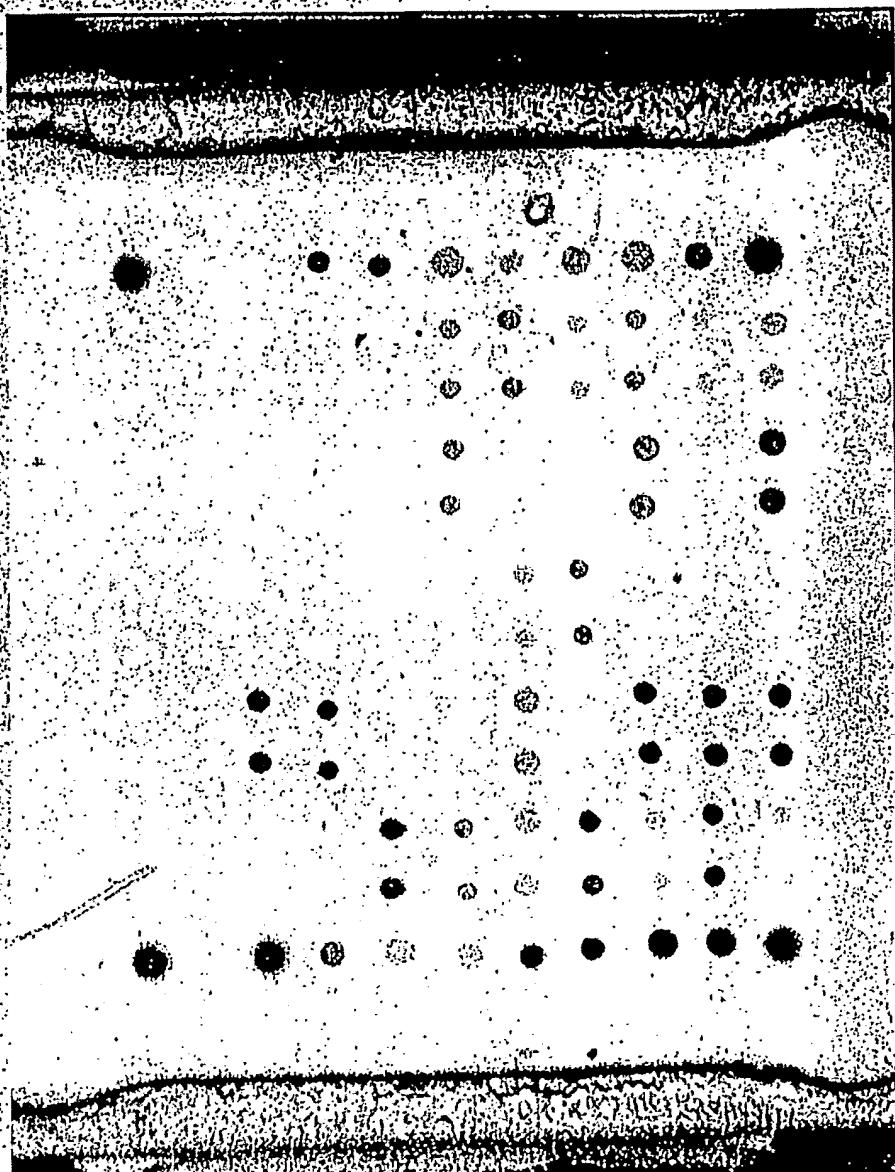


ZW79

*P. aeruginosa* AT-Chip

10/30

Fig.10

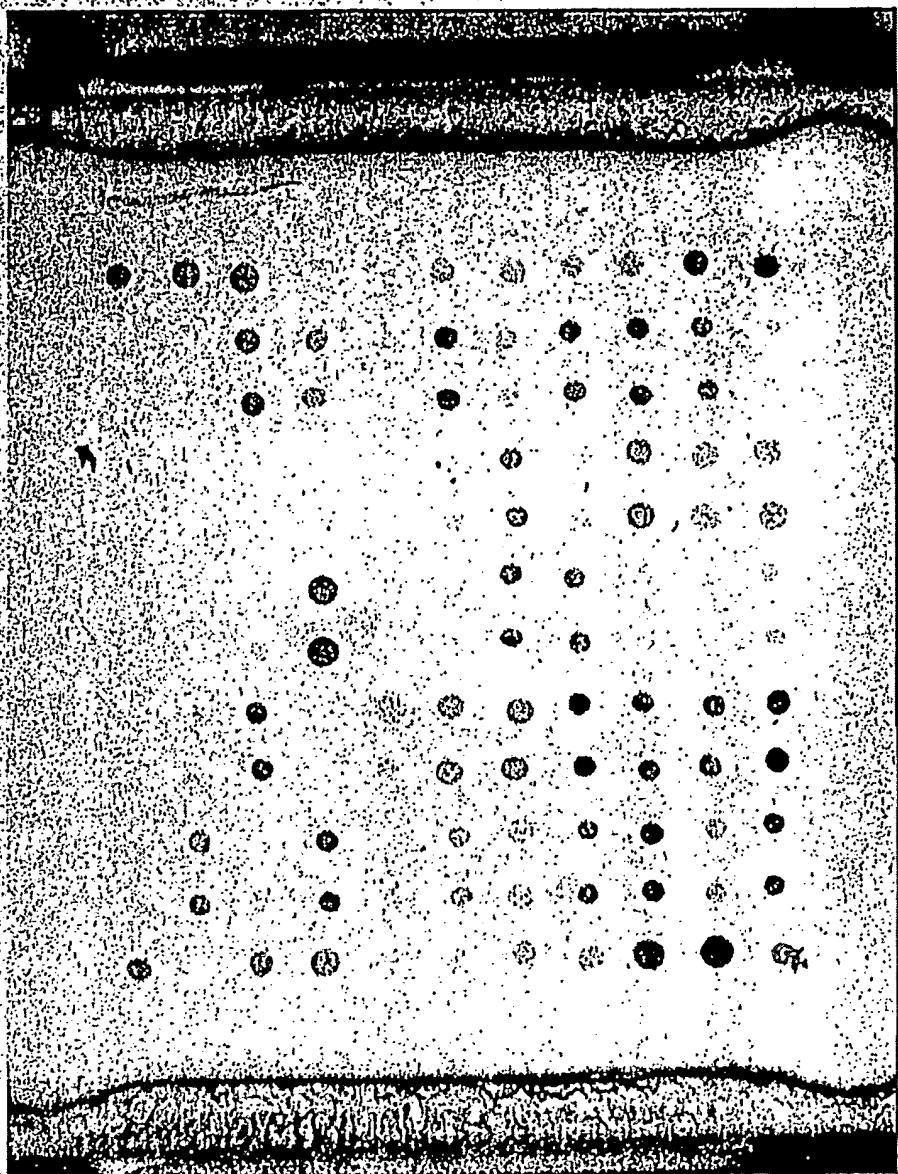


ZW85

*P. aeruginosa* AT-Chip

11/30

Fig.11

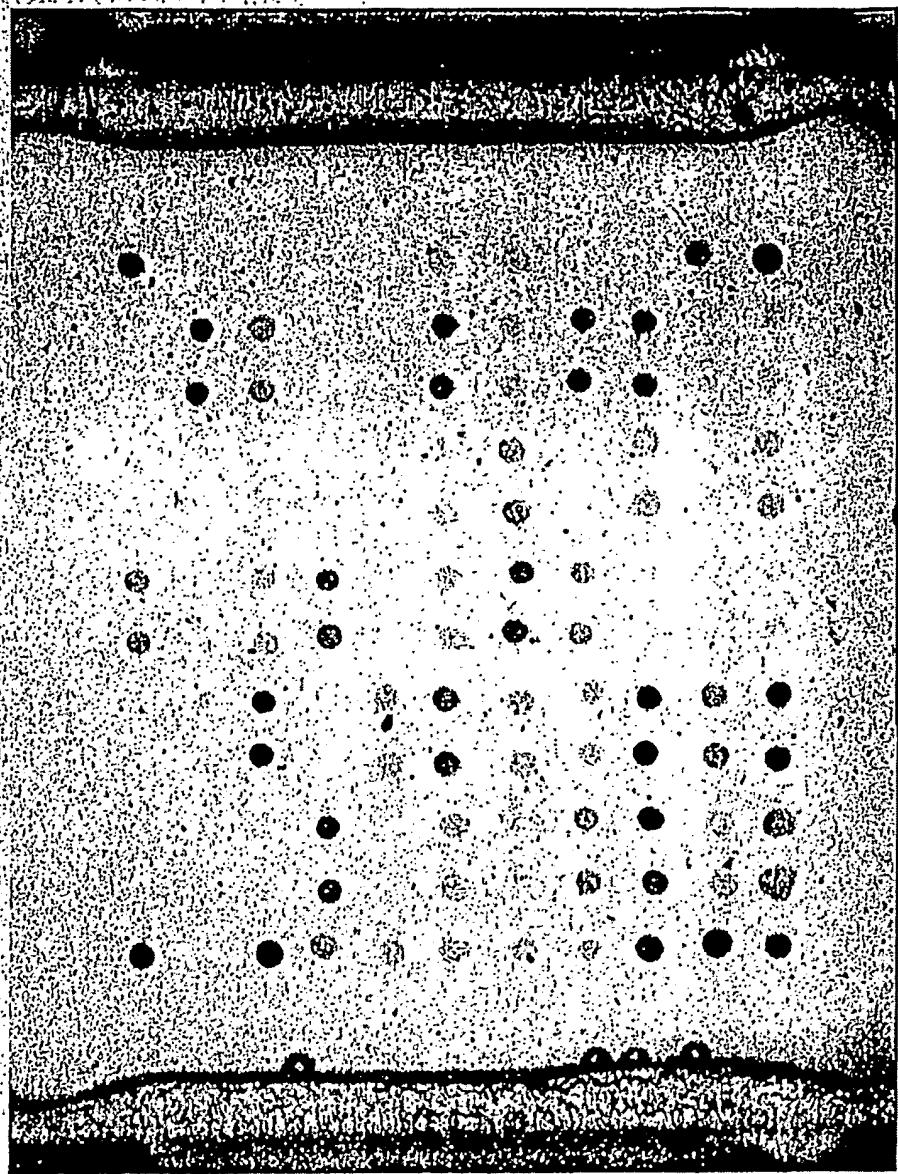


2813A

# *P. aeruginosa* AT-**Chip**

12/30

**Fig.12**

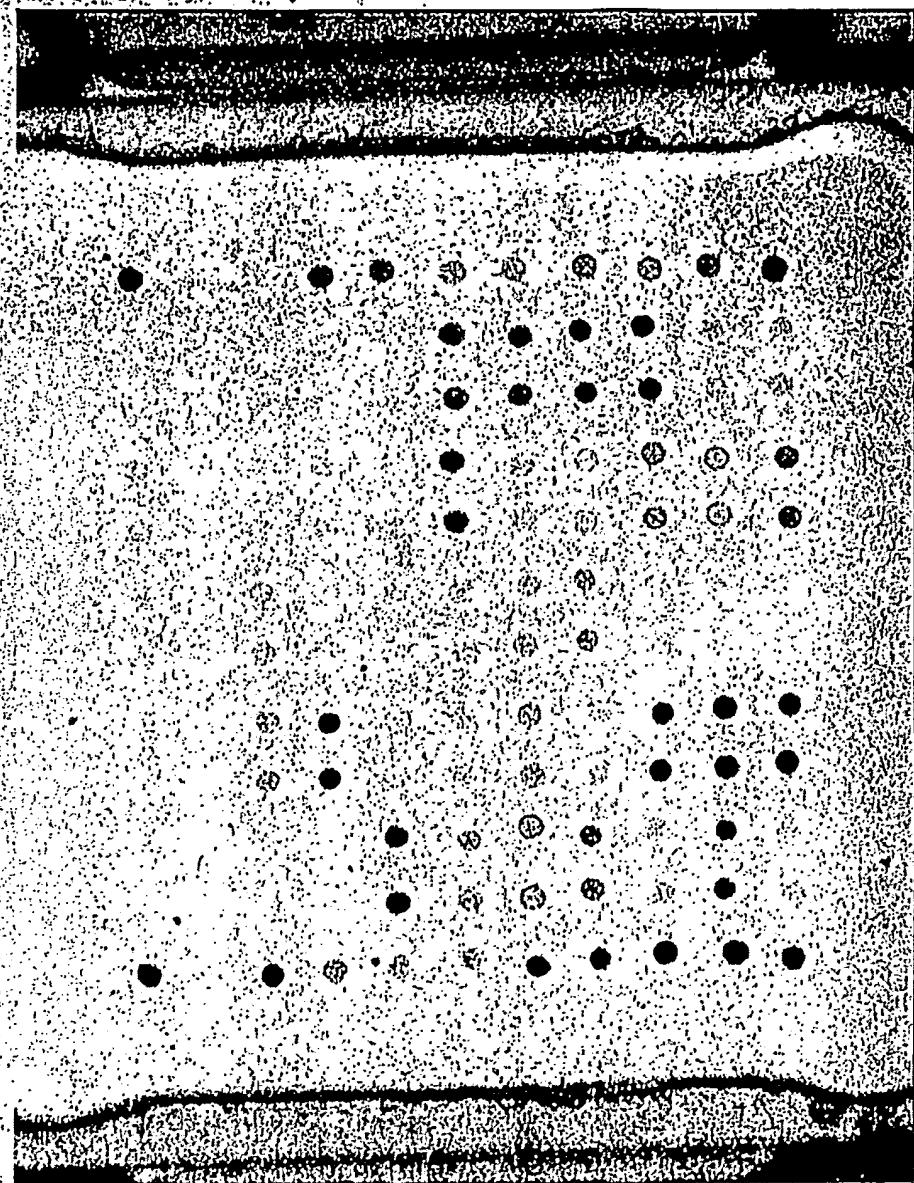


KB1-85

*P. aeruginosa* AT-Chip

13/30

Fig.13

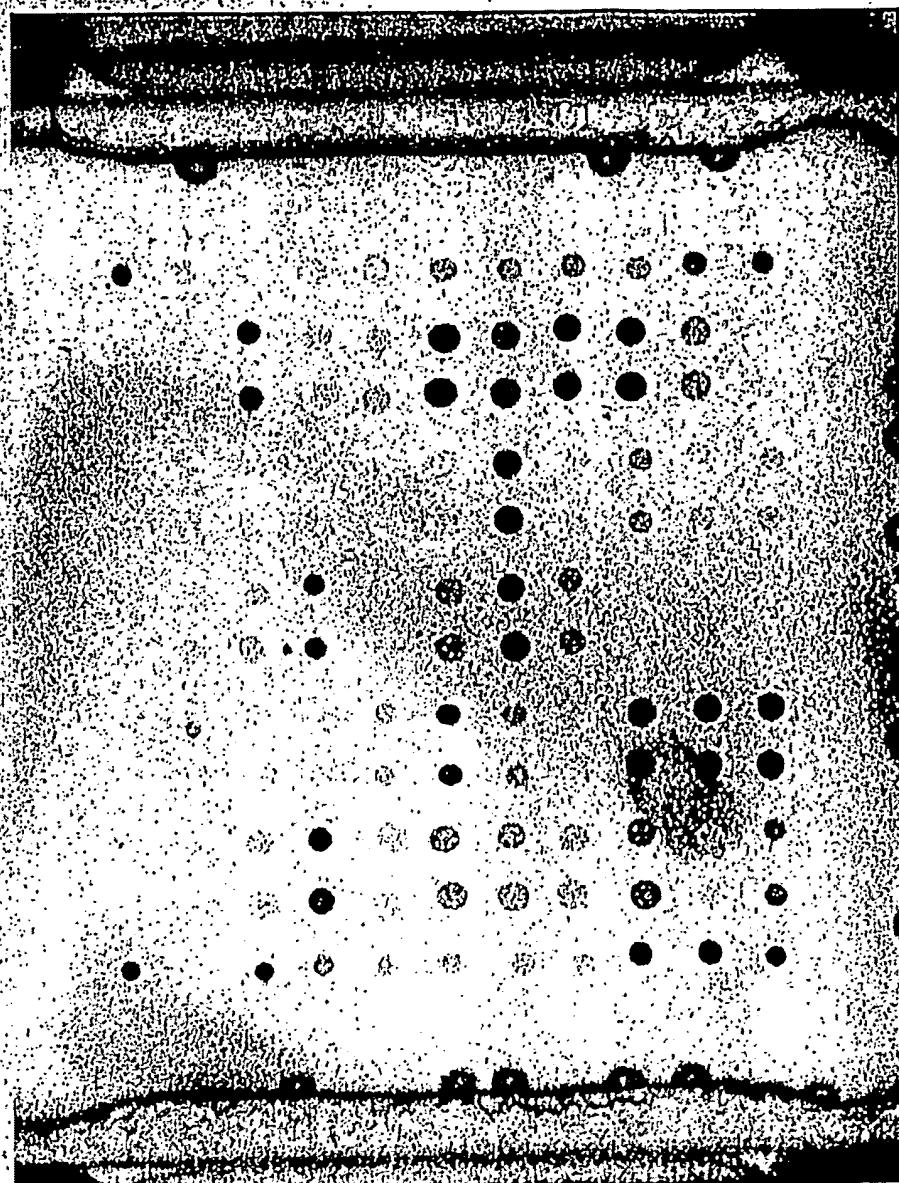


ZW98

# *P. aeruginosa* AT-Chip

14/30

Fig.14

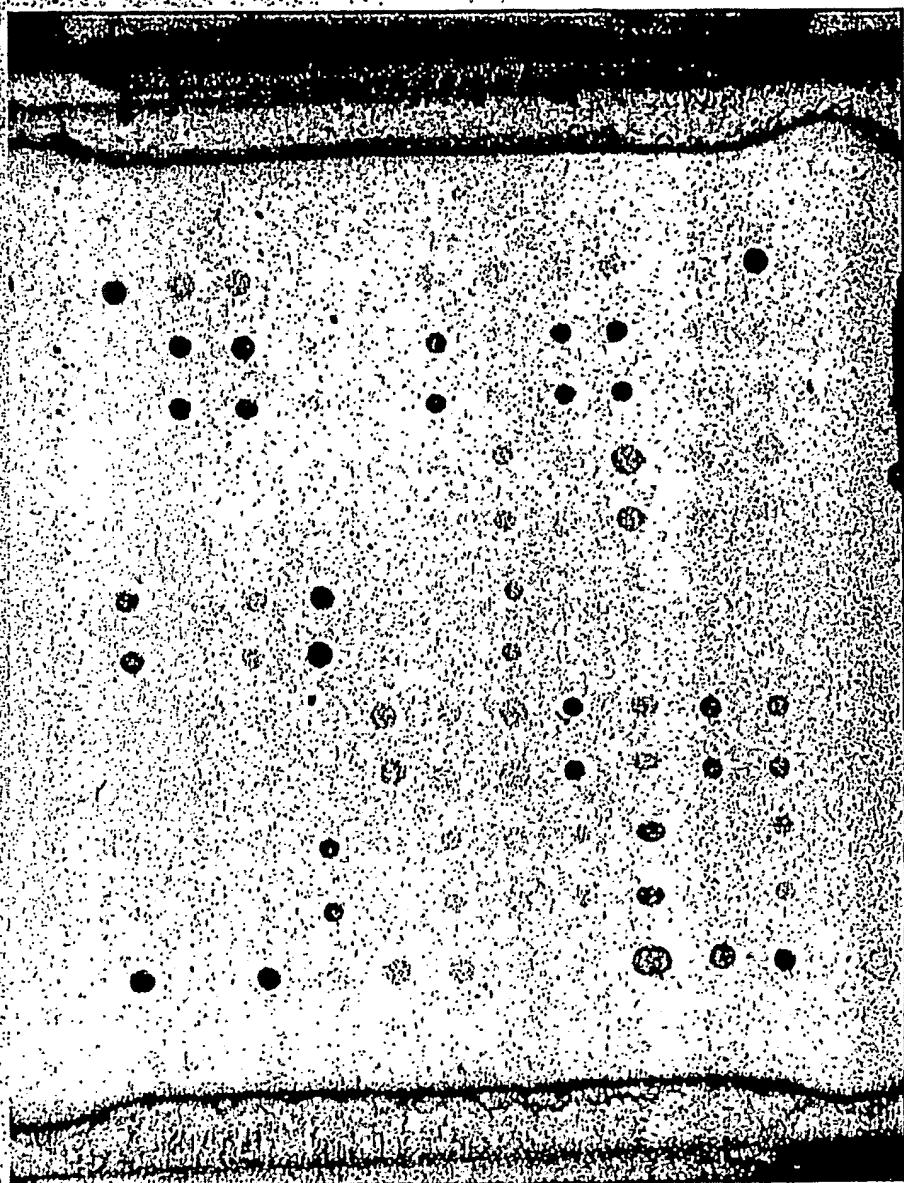


641HD

*P. aeruginosa* AT-Chip

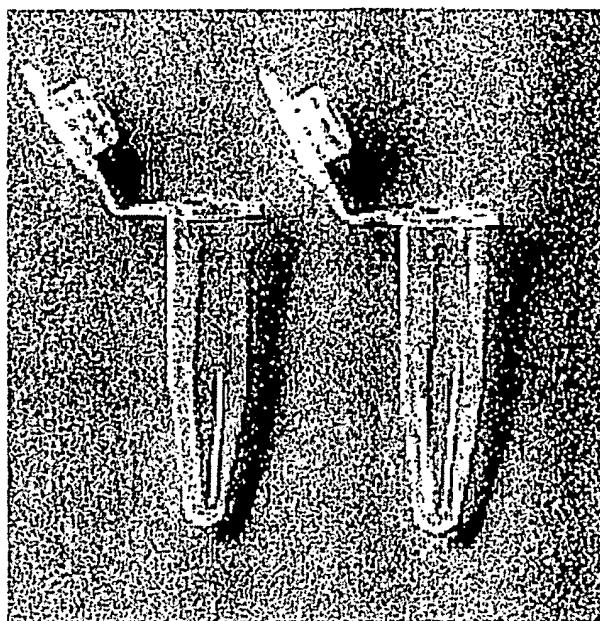
15/30

Fig.15



ATCC15522

**Fig.16**



47-1/23  
ACGGCGATGTCCTGGATTTGG

**Fig.17a**

47-1/39  
CTGAAGAAGGGGGCGCTACGCG

47-2/22  
GCGTACCGGGCAAGGTGATAG

47-2/52  
CTCGGTGAAACATCGGGAGGG

C45/18  
TCATCCAGCAAGCCATTGCGC

C45/60a  
GGAGTCGCTTCCGCCATCG

C45/60b  
TGGAGTCGCTTCCGCCATCG

C46/15  
AAGGGCGTTTCACGCTGACGC

C46/22  
ATCCGGAAGGGCGTTTCACG

C46/88  
TCCACACCTCAGACTCGGCG

C47-1/43  
TATTGACGACCTACCGCGCGC

C47-2/56a  
GCAACTGATGTTGCCAGC

C47-2/56b  
CGCAACTGATGTTGCCAGC

C47-2/59  
ACACGCAACTGATGTTGCC

CIS-4/36  
TGTCCCGGCTCAGTTCAACG

CIS-4/50  
AACACCTTGGCGTTGTCCC

CIS-4/51  
GCAACACCTTGGCGTTGTCCC

CIS-5/4  
TCAAGCTCGTTGTGGACCGC

CIS-5/48  
GTTACGACGGCGTGCCTGTCGG

CSP-1/39a  
ACGCAACGTATTGGCGACCC

CSP-1/39b  
CGCAACGTATTGGCGACCC

**fliAT/28**  
AGCTGATGGTATGCCGTCGC

**fliAT/72**  
CTAGTGATCGCACCGGAGCC

**oriC/20**  
AGCCTCGACACCGGTTCTCG

**oriC/54**  
TCGTTCATCCCCAGGCTTCG

**oriC/59**  
ACCATCTCGTTCATCCCCAGG

**oprL/53**  
TTCTGAGCCCAGGACTGCTCG

**oprL/65**  
TCGACGCGACGGTTCTGAGCC

**fliCb/36**  
TGACGTTCTGCCGGTAGCG

**fliCb/65**  
CAGTAGCGGTACCGGTCTGCG

**fliCb/66**  
CAGTAGCGGTACCGGTCTGCG

**alkAG/27**  
TTCCTCGCCGGCATAGTAGGC

**alkGA/32**

**alkGA/51**  
CGAGGACGAGGCATCTCCGG

**citAG/4**  
GCAGGTAGCAGGTTCCAGG

**citAG/46**  
AACTGTTCCCTCTGCGCGGCG

**citGC/8**  
TGATCGGCTTGGTCTCGCAGG

**citGC/11**  
GCTGATCGGCTTGGTCTCGC

**citGC/75**  
GAGGCCTCTGCTCGTGGTCG

**oprI/12**  
TTTTTCCAGCATGCGCAGGG

**oprI/17**  
GCTGGCTTTCCAGCATGCG

**oprI/22**  
TTGCGGCTGGCTTTCCAGC

**Fig.17b**

**Fig.17c**

am7CA/1  
TTGGGATAGTTGCGGGTTGGC

am7CA/27  
CGTAGGCGATCTTCACCCGC

am7CA/29  
TGGCGTAGGCGATCTTCACCC

am3CT/21  
GGCGAGATAGCCGAACAGGC

am3CT/22  
GCGGCGAGATAGCCGAACAGGG

am3CT/69  
CACTTGCTGCTCCATGAGCC

am2CT/35  
GAGGTCGAGCAGGCTGATGC

am2CT/42  
TAGGTCGCGAGGTAGCAGG

am2CT/92  
GTCCTTCTGCACCGAGTCGG

am1GA/49  
CGCATCTGTCCCTGGGTAGG

am1GA/58  
TCGTCGAGGGCGCATCTTGTCC

am45/1  
ACGTCGAGGTGGGTCTGTTG

am45/96  
GTAGCCTTCGGCATCCAGCG

am6TC/60  
TCGGCATTGGGATAGTTGCGG

GI11/15  
CCTCCTGTCTCATGCCGATGC

GI11/59  
GCATTCGCCACGGAAGGAAGG

GI11/71  
GAAGGCATCATGGCATTGCGC

GI18/62  
GTCATGGGGTTCCCAGAGACC

fliCa/41  
GATCGCGATGTCGACGGTGCC

fliCa/42  
CGATCGCGATGTCGACGGTG

fliCa/46  
TGCCGATCGCGATGTCGACG

**Fig.17d**

SG-1/40  
GACGAATACCCAGCTGCGTGG

SG-1/43  
GCAGACGAATACCCAGCTGCG

SG-4/1  
CGCGACGTCGTGACGTCAGC

SG-4/67  
ACTTCGGCTCTTCGGGCTGG

TB46/21  
AGGTAGAGACTCGGGGGAAACC

TB46/45  
TCGTTTCGGTCATGGCCAGG

TB471/22  
TTCCCGCGACGAACATCCGTGG

TB471/25  
CGCTTCCCGCGACGAACATCCG

TB472/36  
GGATCGCTTCCGATAGGGCAGC

TB472/84  
AGAGGCATGGGTCTGTACCG

TB473/34  
TCTGTCAATCCCCTTGGGG

TB473/41  
AGCCCCCTTCTGTCAATCCCC

TB474/36  
GGCTTCCTACCGAAGGTCAAGG

TB474/41  
TGAGGGCTTCCTACCGAAGG

exoS/31  
TTCAAGGTCAATGGGCAATGCC

exoS/37  
AGTCCCTCAAGGTCAATGGG

exoU/22  
GCCGACTGAGCTGTAGCTCG

exoU/23  
GGCCGACTGAGCTGTAGCTCG

exoU/42  
ACCAGACTGGTCAATGGTGG

flins/2  
CCCGTGTTCCTAGACCTTGC

pKL11/49a  
AGCAGTTACCCACAGCATGG

**Fig.17e**

**pKL11/49b**  
CAGCAGTTACCCACAGCATGG

**pKL3/47**  
CTACACTCCAACCGCTGGTCC

**pKL3/50**  
GACCTACACTCCAACCGCTGG

**pKL3/80**  
TTCCCTTGCTGCCGAGAAAGC

**pKL7/14**  
TAATAGGCGAGCCTGCCGTCC

**47D7nw1a**  
TCCACGCCGAGGGACGTGCC

**47D7nw1b**  
GCTCCACGCCGAGGGACGTGCC

**C46-nw1a**  
CGCGGTGCTGGTTGCGCTGC

**C46-nw1b**  
CCAATGCCAGGGCCAGCGGA

**C46-nw1c**  
CGCTGGCAGTTCCGCTGGCC

**ExoSnw1a**  
CAGGGTCGCCAGCTCGCTGCC

**ExoSnw1b**  
AGGGTCGCCAGCTCGCTCGC

**ExoUnw1a**  
AGTGATCTGCCGCCCTGCC

**ExoUnw1b**  
GTGATCTGCCGCCCTGCC

**OrfA-1**  
GTTCCACAGGCGCTGCCGCC

**OrfA-2**  
GTTCCACAGGCGCTGCCGCC

**OrfA-3**  
CAAAGCCCCCTGGTCGCGCGG

**OrfC-1**  
GCAGCTTTCCACCGCCGGCGG

**OrfI-1**  
AAACTGCCCGCCCCCATCC

**OrfI-2**  
GGAAAAACTGCCCGCCCCCCC

**OrfJ-1**  
ACGCTCGCAGCGCCTCACGCG

*OrfJ-2*  
GGCCTGGCTGCGAACGCTCGC

**Fig.17f**

Fig.18a

no	tube	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spotID's
1	PaS_001	oriCT-C_wt	GAAGCCAGCAATTGGCTTTC	23	52.2	62.4	23	
2	PaS_056	oriCT-T-C_mut_1	GAAGCCAGCAACTGGCTTTC	1	23	56.5	64.2	14,15
3	PaS_057	oprL-T-C_wt_1	GGTGTGCAAGGGTTTCGCCGG	1	23	69.6	69.6	4,5
4	PaS_058	oprL-T-C_mut_1	GGTGTGCAAGGGTTTCGCCGG	1	23	73.9	71.3	16,17
5	PaS_059	flxC_A-T_wt_1	CAAGATCGCCGCAGGGTCAAC	1	22	63.6	65.8	6,7
6	PaS_060	flxC_A-T_mut_1	CAAGATCGCCGCAGGGTCAAC	1	22	63.6	65.8	18,19
7	PaS_061	alkB2_G-A_wt_1	TGCTGCTGGGGGGGGCTGCTAT	1	23	65.2	67.8	8,9
8	PaS_062	alkB2_G-A_mut_1	TGCTGCTGGCAAGGGGGCTAT	1	23	60.9	66.0	20,21
9	PaS_063	alkB2_A-G_wt_1	CCTCGCCCTGTTCCACCGCTCTGG	1	25	72.0	72.8	10,11
10	PaS_064	alkB2_A-G_mut_1	CTCGCCCTGTTCCCGGGCTCTGG	1	24	75.0	73.0	22,23
11	PaS_065	citS_A-G_wt_1	TCGAGCAAATGGCAGAGAAATCCG	1	24	54.2	64.4	26,27
12	PaS_066	citS_A-G_mut_1	CGAGCAAATGGGGAGAAATCCG	1	23	60.9	66.0	38,39
13	PaS_067	citS_G-C_wt_1	GCGGAAAATCTCCTGCACATGATGTT	1	26	46.2	63.2	28,29
14	PaS_068	citS_G-C_mut_1	GCGGAAAATCTCCTCACATGATGTT	1	26	46.2	63.2	40,41
15	PaS_069	oprT-C_wt_1	AGCTCAGCAGACTGCTGACGAG	1	23	60.9	66.0	30,31
16	PaS_070	oprT-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63.6	65.8	42,43
17	PaS_071	ampC_1_G-A_wt_1	AGAGGACGGCCGGGGTGAACGCC	1	25	76.0	74.5	32,33
18	PaS_072	ampC_1_G-A_mut_1	AGAGGACGGCCGGGGTGAACGCC	1	26	73.1	74.3	44,45
19	PaS_019	ampC_2_C-T_wt	GACAAGATGCCCTGACGACC	1	22	63.6	65.8	34,35
		ampC_2_C-T_mut_1	GACAAGATGCCCTGACGACC	1	23	60.9	66.0	45,47
20	PaS_073	ampC_3_C-T_wt	AGCCGACCTACGGCGGGGAG	1	22	77.3	71.4	50,51
21	PaS_021	ampC_3_C-T_mut_1	AGCCGACCTACGGCGGGGAG	1	23	73.9	71.3	62,63
22	PaS_074	ampC_4_G-A_wt_1	CAGCCGACCTATGCCGGGAG	1	23	60.9	66.0	52,53
23	PaS_075	ampC_4_G-A_mut_1	CCGGTCGAACGGCTCATGGAGCA	1	24	58.3	66.1	64,65
24	PaS_076	A_mut_1	GGCGTTGAAACGACTCATGGAGCA	1	22	63.6	65.8	54,55
25	PaS_077	ampC_5_G-C_wt_1	TGGAGCAGCAAGTGTCCCCGGC					

Fig.18b

25	Pa-S_078	ampC_5_G-C_mut_1	TGGAGCAGCAACTGTCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6_T-C_wt	GACAAGACGGGTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_6_T-C_mut_1	ACCAAGACGGGTCCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_025	ampC_7_C-A_wt	GCGACCTGGGCTGGTGTACCT	1	22	68,2	67,7	55,59
30	Pa-S_080	ampC_7_C-A_mut_1	GGGACCTGGGACTGGGTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	flxC_b	GCGACCAACTGAACTCCAACTCG	2	24	58,3	66,1	54,75
32	Pa-S_032	flxC_a	GTGGCTGAACGGCACCTACTICA	2	23	56,5	64,2	86,87
33	Pa-S_033	exoS-1	CGCCCTGGGGTCACTGCTCTCGG	3	22	68,2	67,7	76,77
34	Pa-S_034	exoU	CCCGAGTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
35	Pa-S_038	C-47-1	GGGGATCTCTCCACCTCACGG	4	24	52,2	64,4	57,58,59
36	Pa-S_039	C-47-2	GCTCCGGATTGACATCGTGTAT	4	24	58,3	66,1	90,91
37	Pa-S_040	C-47D7-1	GTAGCCGGAGTCGAGGGAAATCAT	5	24	54,2	64,4	80,81,83
38	Pa-S_041	C-47D7-2	GTGACCATGGAAATCGGGCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_034	C-45	CGAGGAGTTGGAGGGCTTGA	6	24	54,2	64,4	52,53
40	Pa-S_055	C-46	ATATGGACGGAGAACGGCATT	6	24	58,3	66,1	94,95
41	Pa-S_035	C-Insel spez. 4	GGGCCTTCTCTCTTCCAGATGT	7	24	54,2	64,4	58,59
42	Pa-S_036	C-Insel spez.-5	CAGTATGGTAAGGACAGGAAGGCC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATGGGGTCACTCTGGT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCGAACTGGGCTAACCTGGA	9	24	54,2	64,4	100,101
45	Pa-S_045	pKL-7	AATTGATGGCTTCTCAGGCCAGG	9	24	54,2	64,4	112,113
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATACTGGGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TCTCGGTGTCGAGGGATCTCTGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115
49	Pa-S_047	SG17M-1	CCGGTTGCCTCATACCCGGTCTG	11	24	58,3	66,1	104,105
50	Pa-S_048	SG17M-4	AGGGCATTCTCAGTTGACTCAGG	11	24	54,2	64,4	116,117
51	Pa-S_053	fla-Insel-1	ACCTGTGTCGGTGGACTCTT	12	24	58,3	66,1	106,107
52	Pa-S_049	TB-C47-1	AGGTCCCTGACCAACCTCTG	13	24	58,3	66,1	118,119
53	Pa-S_050	TB-C47-2	CCCAACAAATTGCCATTACAGGG	13	24	54,2	64,4	126,127
54	Pa-S_051	TB-C47-3	TCAACAGGCCAGGATACAGGGT	13	24	58,3	66,1	128,129

Fig.18c

55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCCGGTTCTC	13	24	54,2	64,4	130,131
56	Biotin + Cy3-marker							1,12,97,121,132
57	Pa-S_081	oriC T-C_wt_1	AGCCCAGCAATTGCCTGTTCTCCG	1	25	65,6	56	
58	Pa-S_082	oriC T-C_mut_2	AGCCCAGCAACTGCCTGTTCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGGGGGGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGGGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	oprl T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGGAG		27	64,6	56	
62	Pa-S_086	oprl T-C_mut_2	GAAGGCTCAGGAGACCCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGCCGGGTGACGCC		19	70,2	84	
		ampC_1 G- ampC_1 G-						
64	Pa-S_088	A_mut_2	AGGGCCGCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1	GCGGACCTAACGGCCGGGC		19	68,4	84	
		ampC_3 C- ampC_3 C-						
66	Pa-S_090	T_mut_2	AGCCGACCTATGCCGGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCGAACGGCTCATGGAGCAGCA		24	65	58	
		ampC_4 G- ampC_4 G-						
68	Pa-S_092	A_mut_2	GTTCGAACGGACTCATGGAGCAGAAG		26	63,5	54	
69	Pa-S_093	exoS-T_1	CAGGCCAGTCAGGACGGCA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCGTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTACGGCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_ofrA	CGCTGGAGGGTATGTTCGGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_ofrC	CGTACTCAGCTTCTCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_ofrI	CCTGGACCTCTCCAAGGTTGCCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_ofrJ	GCATTCCGACGACCAAAAGGC		24	64,2	58	

group "mother"

Fig.19a

well- no	tube	name	5'-3'-sequence	group	length	GC- content [%]	Tm [°C]	spot- ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCCCAGCAATTGGGTGTTTC	1	23	56,5	64,2	14,15
2	Pa-S_056	oriC T-C_mut_1	GAAGCCCCAGCAACTGGGTGTTTC	1	25	65,6	56	13,25
57	Pa-S_081	oriC T-C_wt_1	AGCCCAAGCAATTGGGTGTTTC	1	24	65,1	58	37,49
58	Pa-S_082	oriC T-C_mut_2	AGCCCAAGCAACTGGGTGTTTC	1	23	69,6	69,6	4,5
3	Pa-S_057	oprL T-C_wt_1	GGTGGCTGCAGGGGTGTTTC	1	23	73,9	71,3	16,17
4	Pa-S_058	oprL T-C_mut_1	GGTGGCTGCAGGGGTGTTTC	1	22	63,6	65,8	6,7
5	Pa-S_059	fliC a A-T_wt_1	CAAGATGCCGCAGGGTCAAC	1	22	63,6	65,8	18,19
6	Pa-S_050	fliC a A-T_mut_1	CAAGATGCCGCAGGGTCAAC	1	19	67,4	79	8,9
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGGGGGTGTGC	1	21	67,3	67	20,21
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGGGGTGTGC	1	25	72,0	72,8	10,11
9	Pa-S_063	alkB2 A-G_wt_1	CCTCGCCCTGTTCCACCGCTCTGG	1	24	75,0	73,0	22,23
10	Pa-S_064	alkB2 A-G_mut_1	CTCGCCCTGTTCCGGCTCTGG	1	24	54,2	64,4	26,27
11	Pa-S_065	ctsA-G_wt_1	TGAGGCAACTGGCAGAGAAATCCG	1	23	60,9	66,0	38,39
12	Pa-S_066	ctsA-G_mut_1	CGAGGCAACTGGGGAGAAATCCG	1	26	46,2	63,2	28,29
13	Pa-S_067	ctsS G-C_wt_1	GCGGAAAAACTCTGCACATGATGTT	1	26	46,2	63,2	40,41
14	Pa-S_068	ctsS G-C_mut_1	GCGGAAAAACTCTCCACATGATGTT	1	23	60,9	66,0	30,31
15	Pa-S_059	oprT-C_wt_1	AGCTCAGCAGACTGCTGACGAG	1	22	63,6	65,8	42,43
16	Pa-S_070	oprT-C_mut_1	AGCTCAGCAGACCCGTGACGAG	1	27	64,6	56	61,73
61	Pa-S_085	oprT-C_wt_2	CAGAAAAGCTCAGGAGACTGCTGACGAG	1	25	64,9	60	24,85
62	Pa-S_086	oprT-C_mut_2	GAAAAGCTCAGGAGACCCGTGACGAG	1	19	70,2	84	32,33
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGGGGGTGACGCC	1	20	69,9	80	44,45
		ampC_1 G- mut_2	ACGGCCGGCCAGGTGACGCC	1	22	63,6	65,8	34,35
64	Pa-S_088	A_mut_2	GACAAAGATGGCCTGACGCC	1	23	60,9	66,0	46,47
19	Pa-S_019	ampC_2 C-T_wt	GACAAAGATGGCCTGACGCC	1	22	77,3	71,4	50,51
		ampC_2 C- mut_1	GACAAAGATGGCCTGACGCC	1	23	73,9	71,3	62,63
20	Pa-S_073	T_mut_1	AGCCGACTACGGCGGGCAG					
21	Pa-S_021	ampC_3 C-T_wt	CAGCCGACCTATGGCGGGCAG					
22	Pa-S_074	T_mut_1						

Fig.19b

65	Pa-S_069	ampC_3_C-T_wt_1	GCCGACCTACGGCGGGC	1	19	68,4	84	36,48
66	Pa-S_090	T_mut_2	AGCCGACCTATGGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_091	ampC_4_G-A_wt_2	GTTCGAACGGCTATGGAGCA	1	24	65	58	52,53
68	Pa-S_092	A_mut_2	GTTGAAACGACTCATGGAGCAAG	1	26	63,5	54	64,65
25	Pa-S_077	ampC_5_G-C_wt_1	TGGAGCACCAAGTGTCCCCGC	1	22	63,6	65,8	54,55
26	Pa-S_078	C_mut_1	TGGAGCACCAACTGTTCCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6_T-C_wt	GAACAAAGACCGGTTCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	C_mut_1	AACAAGACCCGGCTCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7_C-A_wt	GGGACCTGGGCTGTGTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	A_mut_1	GCGACCTGGGCACTGTTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	flic b	GCGACCAACTGAACTCCAACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	flic a	GTCGCTGAACGGCACCTACTCA	2	23	56,5	64,2	66,87
69	Pa-S_093	exoS-1	CGGCCATGACGGACCCGCA	3	20	64,9	70	76,77
34	Pa-S_034	exoU	CGCCCACTTIGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
70	Pa-S_094	exoU_1	AGTGACCGTGCCTTTCAGCAGTCCC	3	24	64,8	58	84,96
35	Pa-S_038	C-47-1	GGCGGATCTCTCCACTCTATGGG	4	22	54,2	64,4	78,79
71	Pa-S_095	47D7-1_1	GTGTCAACGCCATGCTAGCAGC	5	24	65	63	80,81
36	Pa-S_041	47D7-2	GTCGACCTGGGAATCGGCCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGAGTTGGGACCCGGCTTGA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGGAGAACGGGATT	6	24	58,3	66,1	94,95
72	Pa-S_295	C-46_1	CGAAGTCGAGGTGTTGGACCCGC	6	23	64,5	65	108,120
41	Pa-S_035	C-Inselspez-4	GGCCCTTCTCTCTTGGCAATGTT	7	24	54,2	64,4	98,99
42	Pa-S_036	C-Inselspez-5	CAGTATGGTACGGACACGAAGGCC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-4	GGATCACTGGCGTCAATCINGT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGAACCTGGCTATCACCTGCA	9	24	54,2	64,4	100,101
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATAACGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCCTGGTGTGGAGGATTCCTCGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115

**Fig.19c**

49	Pa-S_047	SG17M-1	CCCGTTGCTCATAACCGTTCCCTG	11	24	54,3,66,1,101,105
50	Pa-S_048	SG17M-4	AGGCATTTCTCAGGTGGACTCAGG	11	24	54,2,64,4,116,117
51	Pa-S_053	fla-Insel-1	ACCTGTGTCGGCTGGAGGTATGTT	12	24	58,3,66,1,106,107
54	Pa-S_051	TB-C47-3	TCCACAGGGAGGTACAGGGTG	13	24	58,3,66,1,128,129
55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCCGGTTCTC	13	24	54,2,64,4,130,131
73	Pa-S_097	Fla-Insel-2_ofA	CGCTGGAGGGTATGTCGCCAAGG	14	24	64,8,63,91
74	Pa-S_098	Fla-Insel-2_ofC	CGTACTCAGCTCTCCACCCAGCG	14	24	64,3,63,112,113
75	Pa-S_099	Fla-Insel-2_ofI	CCTGGACCTCTCAAGGTTCGCT	14	24	65,63,118,119
76	Pa-S_100	Fla-Insel-2_ofJ	GCCATTCCGACGACCAAAAGGC	14	24	64,2,58,126,127
56	Biotin + Cy3-marker					1,12,97,121,132

group "mother"

**Fig.20**

Chip: MHH\_P\_aer\_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2 offJ	TB-C47-3	TB-C47-4	marker spot
C-Insel spezifisch-5	Fla-Insel-2 offC	PAGI-1-8	SG17M-4	Fla-Insel-2 offJ	C-46_1	
marker spot	C-Insel spezifisch-4	pKL-3	PAGI-1-1	SG17M-1	fla-Insel-1	C-46_1
mut_2	flc A	exoU	Fla-Insel-2 offA	47D7-2	C-46	exoU_1
oprI T-C	flc B	exoS-1_1	C-47-1	47D7-1_1	C-45	exoU_1
wt_2	mut_1 ampC_3 C-T wt_2	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T wt_2
mut_2	mut_1 cits A-G wt_1	mut_1 cits G-C wt_1	mut_1 oprI T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	mut_1 ampC_3 C-T wt_1
oriC T-C	mut_1 oriC T-C wt_1	mut_1 oriC T-C wt_1	mut_1 oprI T-C wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	marker spot
wt_1	mut_1 oriC T-C wt	mut_1 oprI T-C wt_1	mut_1 fliC a A-T wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	oprI T-C mut_2 marker spot

30/30

Fig.21